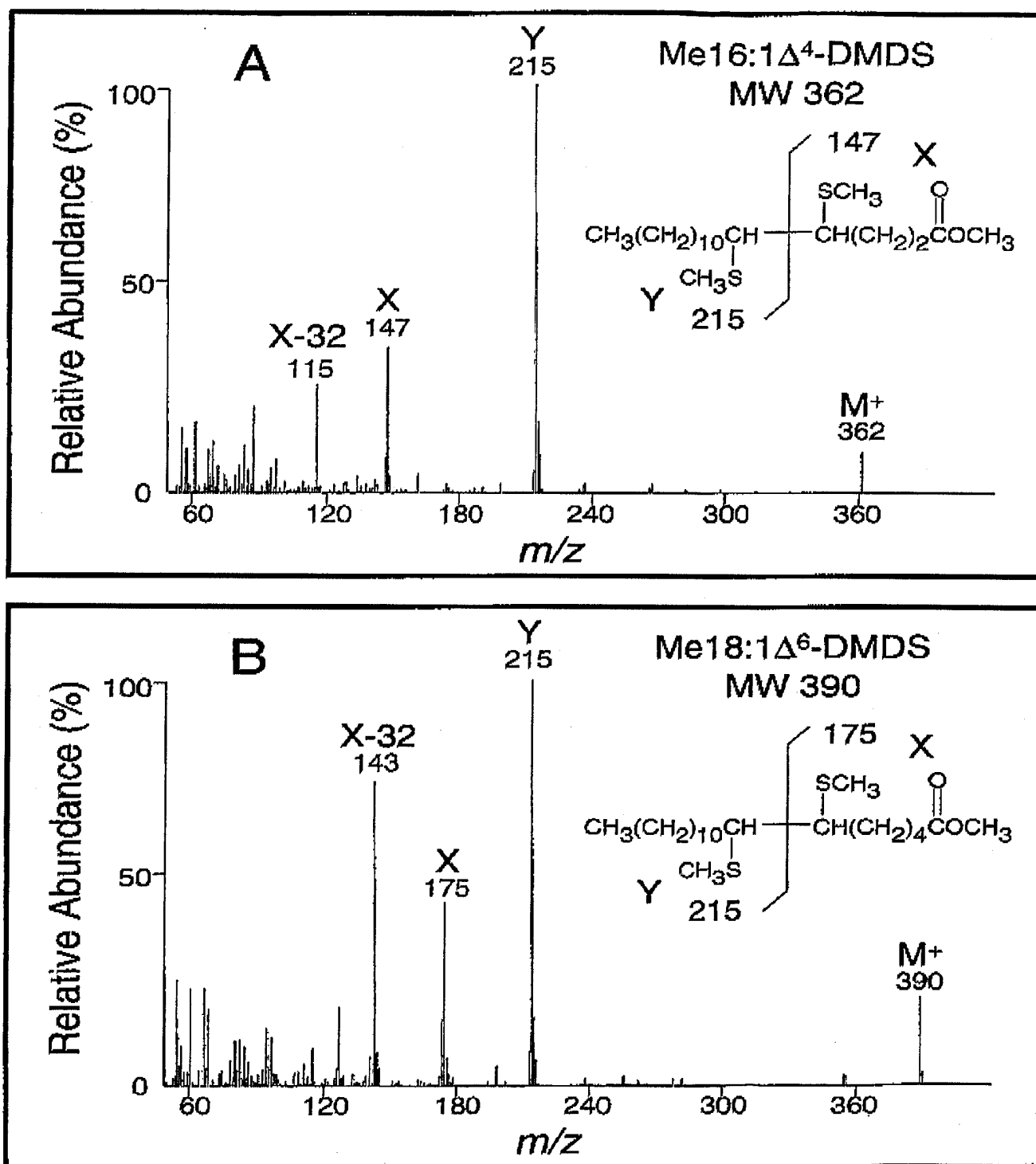APPENDIX A

APPENDIX B

```
#NEXUS
[[Alignment of:]
[Sequence              Start     End     Sequencetype]
[SEQ ID NO 6           (1   >   137)     PROTEIN]
[SEQ ID NO 2           (1   >   394)     PROTEIN]
[417819                (1   >   385)     PROTEIN]
[A47245                (1   >   385)     PROTEIN]

begin data;
   dimensions ntax=4 nchar=398;
   format datatype=Protein interleave gap=- missing='.';
   matrix

SEQ ID NO 6   MA-------------------------------------SVTASSISFTSI--ASSLKQ
SEQ ID NO 2   MALKLN----FQCKKNHPAAFAKSPLFVTRVSSPRVFMASTVNSNSMVLDNLKSPPNLQV
417819        MAMKLNALMTLQCPKRN--MFTRIAPPQAGRVRSKVSMASTLHASPLVFDKLKAGR----
A47245        MAMKLNALMTLQCPKRN--MFTRIAPPQAGRVRSKVSMASTLHASPLVFDKLKAGR----

SEQ ID NO 6   NQGLAKSSISL--SVNG-------------------------------------KSFRS---
SEQ ID NO 2   THSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVRELRERAK
417819        -----PEVDELFNSLEGWARDNILVHLKSVENSWQPQDYLPDPTSDAFEDQVKEMRERAK
A47245        -----PEVDELFNSLEGWARDNILVHLKSVENSWQPQDYLPDPTSDAFEDQVKEMRERAK

SEQ ID NO 6   ------------------------------------------------------------
SEQ ID NO 2   EIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTAEENRHGD
417819        DIPDEYFVVLVGDMITEEALPTYMSMLNRCDGIKDDTGAQPTSWATWTRAWTAEENRHGD
A47245        DIPDEYFVVLVGDMITEEALPTYMSMLNRCDGIKDDTGAQPTSWATWTRAWTAEENRHGD

SEQ ID NO 6   ---------------LRLLSAPLRFRVSCAAKPAT-------------------------
SEQ ID NO 2   LLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERATFISHANTAK
417819        LLNKYLYLSGRVDMRMIEKTIQYLIGSGMDTKTENCPYMGFIYTSFQERATFISHANTAK
A47245        LLNKYLYLSGRVDMRMIEKTIQYLIGSGMDTKTENCPYMGFIYTSFQERATFISHANTAK

SEQ ID NO 6   ----------VDKVC-------------------------------EIVRKQLALPAD
SEQ ID NO 2   LAQHYGDIQNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRKKITMPAH
417819        LAQHYGDKNLAQVCGNIASDEKRHATAYTKIVEKLAEIDPDTTVIAFSDMMRKKIQMPAH
A47245        LAQHYGDKNLAQVCGNIASDEKRHATAYTKIVEKLAEIDPDTTVIAFSDMMRKKIQMPAH

SEQ ID NO 6   SAVTGESK-----FAALGAD-----SLDTVEIVMGLEEEF------GISVEEESAQT-IA
SEQ ID NO 2   LMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLVDKWNVERLTGLSDEGRKAQEYVC
417819        AMYDGSDDMLFKHFTAVAQQIGVYSAWDYCDIIDFLVDKWNVAKMTGLSGEGRKAQEYVC
A47245        AMYDGSDDMLFKHFTAVAQQIGVYSAWDYCDIIDFLVDKWNVAKMTGLSGEGRKAQEYVC

SEQ ID NO 6   TVQDAADLIEKLVEKKE-----------------------
SEQ ID NO 2   ELGPKIRRVEEKVQGKEKKKKAEHPVSFSWIFNRELKI
417819        SLAAKIRRVEEKVQGKEKK--AVLPVAFSWIFNRQIII
A47245        SLAAKIRRVEEKVQGKEKK--AVLPVAFSWIFNRQIII
```

Pair Distances of Untitled ClustalV (PAM250)
        Percent Similarity in upper triangle
        Percent Divergence in lower triangle

	SEQ ID NO 6	SEQ ID NO 2	417819	A47245	
SEQ ID NO 6	***	14.6	14.6	14.6	SEQ ID NO 6
SEQ ID NO 2	232.0	***	73.8	73.8	SEQ ID NO 2
417819	191.3	26.6	***	100.0	417819